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7. The method of claim 5 wherein said translational initiation region includes a prokaryotic secretion signal sequence.

SUB F1) 8. The method of claim 7 wherein said secretion signal sequence is selected from the group consisting of STII, OmpA, PhoE, LamB, MBP and PhoA.

9. The method of claim 8 wherein said signal sequence is selected from the group consisting of STII, PhoE and LamB.

10. The method of claim 9 wherein said signal sequence is STII.

11. The method of claim 9 wherein said signal sequence is LamB.

12. The method of claim 9 wherein said signal sequence is PhoE.

13. A nucleic acid encoding a translational initiation region variant, wherein the translational strength of said variant translational initiation region is less than the translational strength of the wild-type translational initiation region, wherein said translational initiation region includes a prokaryotic secretion signal sequence selected from the group consisting of STII, OmpA, PheE, LamB, MBP and PhoA.

C1 SUB F1) CONT 14. A nucleic acid encoding a polypeptide operably linked to a translational initiation region variant, wherein the translational strength of said variant translational initiation region is less than the translational strength of the wild-type translational initiation region.

15. The nucleic acid of claim 14 wherein said translational initiation region includes a prokaryotic secretion signal sequence.

SUB F1) 16. The nucleic acid of claim 15 wherein said translational initiation region includes a signal sequence selected from the group consisting of STII, OmpA, PhoE, LamB, MBP and PhoA.

17. The nucleic acid of claim 16 wherein said signal sequence is selected from the group consisting of STII, PhoE and LamB.

18. The nucleic acid of claim 17 wherein said signal sequence is STII.

19. The nucleic acid of claim 17 wherein said signal sequence is LamB.

20. The nucleic acid of claim 17 wherein said signal sequence is PhoE.